IN THE CLAIMS

Please amend the claims as follows:

1-29. (Canceled)

30. (Currently Amended) A process for the production of a lipooligosaccharide (LOS) which comprises the steps of:

(a) growing in a culture medium *Salmonella minnesota* bacteria comprising (i) a core lipid structure containing a terminal heptose and (ii) a DNA sequence encoding an Undecaprenyl-phosphate N-acetyl glucosaminyl phosphate transferase (*rfe*) that is part of the *Salmonella minnesota* genome, and (iii) an isolated DNA sequence encoding a naturally-occurring lipooligosaccharide-synthesis gene G polypeptide (LsgG) from *Haemophilus influenzae*, wherein the DNA sequence encoding *rfe* is regulated by LsgG such that the LOS is synthesized by the addition of an acceptor molecule to the terminal heptose molecule; and

(b) recovering the LOS from the culture medium.

Claims 31-33. (Cancelled)

34. (Previously presented) The process of claim 30, wherein the acceptor molecule is N-acetylglucosamine.

Claims 35-36. (Cancelled).

37. (Previously presented) The process of claim 30, wherein the isolated DNA sequence encoding the LsgG is comprised in a vector.

38. (Previously presented) The process of claim 30, wherein the bacteria further comprise a glycosyltransferase.

39. (Currently Amended) A process for the production of a complex carbohydrate comprising the steps of:

(a) growing in a culture medium *Salmonella minnesota* bacteria comprising (i) a core lipid structure containing a terminal heptose and (ii) a DNA sequence encoding an Undecaprenyl-phosphate N-acetyl glucosaminyl phosphate transferase (*rfe*) that is part of the *Salmonella minnesota* genome, and (iii) an isolated DNA sequence encoding a naturally-occurring lipooligosaccharide-synthesis gene G polypeptide (LsgG) from *Haemophilus influenzae*, wherein the DNA sequence encoding *rfe* is regulated by LsgG such that a complex carbohydrate is synthesized by the addition of an acceptor molecule to the heptose molecule; and

(b) recovering the complex carbohydrate from the culture medium.

Claims 40-42. (Cancelled)

43. (Previously presented) The process of claim 39, wherein the acceptor molecule is N-acetylglucosamine.

Claims 44-45. (Cancelled)

46. (Previously presented) The process of claim 39, wherein the isolated DNA sequence encoding LsgG is contained in a vector.

47. (Previously presented) The process of claim 39, wherein the bacteria further comprise a glycosyltransferase.

48. (Currently Amended) A method comprising modifying a terminal heptose of a lipopolysaccharide (LPS) or lipooligosaccharide (LOS) core structure of a *Salmonella minnesota* bacterium, wherein the bacterium comprises a polynucleotide encoding an Undecaprenyl-phosphate N-acetyl glucosaminyl phosphate transferase (*rfe*) that is part of the *Salmonella minnesota* genome and an isolated naturally-occurring DNA sequence encoding a lipooligosaccharide-synthesis gene G polypeptide (LsgG) from *Haemophilus*

influenzae, wherein the polynucleotide encoding *rfe* is regulated by lipooligosaccharide-synthesis gene G polypeptide (LsgG) from *Haemophilus influenzae* such that an N-acetyl glucosamine is added onto the terminal heptose so as to modify the terminal heptose.

Claims 49-53. (Cancelled)

54. (Previously presented) The method of claim 48, wherein a polynucleotide encoding the LsgG is comprised in a vector.

55. (Previously presented) The method of claim 48, wherein the bacteria further comprise a glycosyltransferase.

56. (Previously presented) The process of claim 38, wherein the glycosyltransferase is a *Haemophilus influenzae* glycosyltransferase.

57. (Previously presented) The process of claim 47, wherein the glycosyltransferase is a *Haemophilus influenzae* glycosyltransferase.

58. (Previously presented) The method of claim 55, wherein the glycosyltransferase is a *Haemophilus influenzae* glycosyltransferase.

59. (New) A process for the production of a lipooligosaccharide (LOS) which comprises the steps of:

(a) growing in a culture medium *Salmonella minnesota* bacteria comprising (i) a core lipid structure containing a terminal heptose and (ii) a DNA sequence encoding an Undecaprenyl-phosphate N-acetyl glucosaminyl phosphate transferase (*rfe*) that is part of the *Salmonella minnesota* genome, and (iii) an isolated DNA sequence encoding a lipooligosaccharide-synthesis gene G polypeptide (LsgG) from *Haemophilus influenzae*, wherein the DNA sequence encoding *rfe* is regulated by LsgG such that the LOS is synthesized by the addition of an acceptor molecule to the terminal heptose molecule, and wherein the isolated DNA sequence encoding a lipooligosaccharide-synthesis gene G

polypeptide (LsgG) from *Haemophilus influenzae* is encoded by pGEMLOS-4, pGEMLOS-5 or pGEMLOS-7; and

(b) recovering the LOS from the culture medium.

60. (New) The process of claim 59, wherein the acceptor molecule is N-acetylglucosamine.

61. (New) The process of claim 59, wherein the isolated DNA sequence encoding the LsgG is comprised in a vector.

62. (New) The process of claim 59, wherein the bacteria further comprise a glycosyltransferase.

63. (New) The process of claim 62, wherein the glycosyltransferase is a *Haemophilus influenzae* glycosyltransferase.

64. (New) A process for the production of a complex carbohydrate comprising the steps of:

(a) growing in a culture medium *Salmonella minnesota* bacteria comprising (i) a core lipid structure containing a terminal heptose and (ii) a DNA sequence encoding an Undecaprenyl-phosphate N-acetyl glucosaminyl phosphate transferase (*rfe*) that is part of the *Salmonella minnesota* genome, and (iii) an isolated DNA sequence encoding a lipooligosaccharide-synthesis gene G polypeptide (LsgG) from *Haemophilus influenzae*, wherein the DNA sequence encoding *rfe* is regulated by LsgG such that a complex carbohydrate is synthesized by the addition of an acceptor molecule to the heptose molecule, and wherein the isolated DNA sequence encoding a lipooligosaccharide-synthesis gene G polypeptide (LsgG) from *Haemophilus influenzae* is encoded by pGEMLOS-4, pGEMLOS-5 or pGEMLOS-7; and

(b) recovering the complex carbohydrate from the culture medium.

65. (New) The process of claim 64, wherein the acceptor molecule is N-acetylglucosamine.

66. (New) The process of claim 64, wherein the isolated DNA sequence encoding LsgG is contained in a vector.

67. (New) The process of claim 64, wherein the bacteria further comprise a glycosyltransferase.

68. (New) The process of claim 67, wherein the glycosyltransferase is a *Haemophilus influenzae* glycosyltransferase.

69. (New) A method comprising modifying a terminal heptose of a lipopolysaccharide (LPS) or lipooligosaccharide (LOS) core structure of a *Salmonella minnesota* bacterium, wherein the bacterium comprises a polynucleotide encoding an Undecaprenyl-phosphate N-acetyl glucosaminyl phosphate transferase (*rfe*) that is part of the *Salmonella minnesota* genome and an isolated DNA sequence encoding a lipooligosaccharide-synthesis gene G polypeptide (LsgG) from *Haemophilus influenzae*, wherein the polynucleotide encoding *rfe* is regulated by lipooligosaccharide-synthesis gene G polypeptide (LsgG) from *Haemophilus influenzae* such that an N-acetyl glucosamine is added onto the terminal heptose so as to modify the terminal heptose, and wherein the isolated DNA sequence encoding a lipooligosaccharide-synthesis gene G polypeptide (LsgG) from *Haemophilus influenzae* is encoded by pGEMLOS-4, pGEMLOS-5 or pGEMLOS-7.

70. (New) The method of claim 69, wherein a polynucleotide encoding the LsgG is comprised in a vector.

71. (New) The method of claim 69, wherein the bacteria further comprise a glycosyltransferase.

72. (New) The method of claim 71, wherein the glycosyltransferase is a *Haemophilus influenzae* glycosyltransferase.